

506

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/502,394
Source: PCR
Date Processed by STIC: 1/13/06

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PCT

RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/502,394

TIME: 10:04:26

Input Set : A:\3U 9U 901 PCT.ST25 sequence list.txt

Output Set: N:\CRF4\01132006\J502394.raw

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5 <110> APPLICANT: ORIGENE TECHNOLOGIES INC
7 <120> TITLE OF INVENTION: CANCER GENES
9 <130> FILE REFERENCE: 3U 9U 901 PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/502,394
C--> 11 <141> CURRENT FILING DATE: 2004-07-26
11 <150> PRIOR APPLICATION NUMBER: US 10/054,935
12 <151> PRIOR FILING DATE: 2002-01-25
14 <150> PRIOR APPLICATION NUMBER: US 60/356,130
15 <151> PRIOR FILING DATE: 2002-02-14
17 <150> PRIOR APPLICATION NUMBER: US 10/102,946
18 <151> PRIOR FILING DATE: 2002-03-22
20 <150> PRIOR APPLICATION NUMBER: US 10/117,229
21 <151> PRIOR FILING DATE: 2002-04-08
23 <150> PRIOR APPLICATION NUMBER: US 10/144,198
24 <151> PRIOR FILING DATE: 2002-05-14
26 <150> PRIOR APPLICATION NUMBER: US 10/197,824
27 <151> PRIOR FILING DATE: 2002-07-19
29 <160> NUMBER OF SEQ ID NOS: 102
31 <170> SOFTWARE: PatentIn version 3.1
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 6726
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (367)..(5061)
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52 cctcgtcgtc gtcctcctgg gtccaggcgc ggggacagag tcgcctcccc cgctcctcgg 300
54 agcggcggcg gcggtggtgc ctccggactg cacttgcgaa gggagcttgg ggaggaatag 360
56 tacaaa atg tca aaa att aga agg aag gtc aca gtg gaa aat acc aag 408
57 Met Ser Lys Ile Arg Arg Lys Val Thr Val Glu Asn Thr Lys
58 1 5 10
60 act ata tct gat agc aca tcc cga aga ccc agt gta ttt gag agg ctt 456
61 Thr Ile Ser Asp Ser Thr Ser Arg Arg Pro Ser Val Phe Glu Arg Leu
62 15 20 25 30
64 gga ccc agc act ggc agt aca gca gag aca cag tgc cgt aac tgg ctg 504
65 Gly Pro Ser Thr Gly Ser Thr Ala Glu Thr Gln Cys Arg Asn Trp Leu
66 35 40 45

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68 aag act ggc aac tgc ctc tat gga aac aca tgt aga ttc gta cat ggc      552
69 Lys Thr Gly Asn Cys Leu Tyr Gly Asn Thr Cys Arg Phe Val His Gly
70          50          55          60
72 cct tca cct cgt ggt aaa ggt tat agc agc aat tat aga agg tca cca      600
73 Pro Ser Pro Arg Gly Lys Gly Tyr Ser Ser Asn Tyr Arg Arg Ser Pro
74          65          70          75
76 gaa aga cct aca ggg gat ctt aga gaa aga atg aag aac aag cgc caa      648
77 Glu Arg Pro Thr Gly Asp Leu Arg Glu Arg Met Lys Asn Lys Arg Gln
78          80          85          90
80 gac gtg gac act gag ccc cag aaa cga aat aca gag gag tca tcc tca      696
81 Asp Val Asp Thr Glu Pro Gln Lys Arg Asn Thr Glu Glu Ser Ser Ser
82 95          100          105          110
84 cct gtt agg aaa gaa tct tca aga ggg aga cat agg gaa aag gaa gac      744
85 Pro Val Arg Lys Glu Ser Ser Arg Gly Arg His Arg Glu Lys Glu Asp
86          115          120          125
88 ata aaa atc act aag gaa aga act cca gaa agt gaa gaa gaa aat gta      792
89 Ile Lys Ile Thr Lys Glu Arg Thr Pro Glu Ser Glu Glu Glu Asn Val
90          130          135          140
92 gaa tgg gaa act aat aga gat gat tct gac aat gga gat att aat tat      840
93 Glu Trp Glu Thr Asn Arg Asp Asp Ser Asp Asn Gly Asp Ile Asn Tyr
94          145          150          155
96 gat tat gtt cat gaa ttg tca ttg gaa atg aag cgt cag aag ata cag      888
97 Asp Tyr Val His Glu Leu Ser Leu Glu Met Lys Arg Gln Lys Ile Gln
98          160          165          170
100 agg gaa tta atg aag ctg gaa caa gaa aac atg gag aag aga gaa gaa      936
101 Arg Glu Leu Met Lys Leu Glu Gln Glu Asn Met Glu Lys Arg Glu Glu
102 175          180          185          190
104 att atc att aaa aag gag gtt tca cca gaa gtg gtt aga tca aaa ttg      984
105 Ile Ile Ile Lys Lys Glu Val Ser Pro Glu Val Val Arg Ser Lys Leu
106          195          200          205
108 tcc ccg tca cct tct cta aga aag tct agc aaa tct ccg aag cga aaa      1032
109 Ser Pro Ser Pro Ser Leu Arg Lys Ser Ser Lys Ser Pro Lys Arg Lys
110          210          215          220
112 tca agc ccg aag tcg tct tca gct agc aag aaa gat agg aag aca tct      1080
113 Ser Ser Pro Lys Ser Ser Ser Ala Ser Lys Lys Asp Arg Lys Thr Ser
114          225          230          235
116 gca gta tct tct ccc ctg ttg gac cag cag aga aat tca aaa acc aac      1128
117 Ala Val Ser Ser Pro Leu Leu Asp Gln Gln Arg Asn Ser Lys Thr Asn
118          240          245          250
120 caa agt aaa aag aaa gga cca cgt act cct agt cca ccc cct cct ata      1176
121 Gln Ser Lys Lys Lys Gly Pro Arg Thr Pro Ser Pro Pro Pro Pro Ile
122 255          260          265          270
124 cca gaa gat atc gct ctg ggg aaa aaa tac aaa gaa aaa tat aaa gta      1224
125 Pro Glu Asp Ile Ala Leu Gly Lys Lys Tyr Lys Glu Lys Tyr Lys Val
126          275          280          285
128 aaa gac agg ata gaa gaa aaa aca aga gat gga aag gac aga gga cga      1272
129 Lys Asp Arg Ile Glu Glu Lys Thr Arg Asp Gly Lys Asp Arg Gly Arg
130          290          295          300
132 gat ttt gaa cga caa aga gaa aag aga gac aag cca agg tct act tcc      1320

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133 Asp Phe Glu Arg Gln Arg Glu Lys Arg Asp Lys Pro Arg Ser Thr Ser
134      305      310      315
136 cca gca gga cag cat cat tct cct ata tct tct aga cat cac tca tct      1368
137 Pro Ala Gly Gln His His Ser Pro Ile Ser Ser Arg His His Ser Ser
138      320      325      330
140 tcc tca caa tca gga tca tct att caa aga cat tct cct tct cct cgt      1416
141 Ser Ser Gln Ser Gly Ser Ser Ile Gln Arg His Ser Pro Ser Pro Arg
142 335      340      345      350
144 cga aaa aga act cct tca cca tct tat cag cgg aca cta act cca cct      1464
145 Arg Lys Arg Thr Pro Ser Pro Ser Tyr Gln Arg Thr Leu Thr Pro Pro
146      355      360      365
148 tta cga cgc tct gcc tct cct tat cct tca cat tct ttg tcg tct ccc      1512
149 Leu Arg Arg Ser Ala Ser Pro Tyr Pro Ser His Ser Leu Ser Ser Pro
150      370      375      380
152 cag aga aag cag agt cct cca aga cat cgc tct cca atg cga gag aaa      1560
153 Gln Arg Lys Gln Ser Pro Pro Arg His Arg Ser Pro Met Arg Glu Lys
154      385      390      395
156 ggg aga cat gat cat gaa cga act tca cag tct cat gat cga cgc cac      1608
157 Gly Arg His Asp His Glu Arg Thr Ser Gln Ser His Asp Arg Arg His
158      400      405      410
160 gaa agg agg gaa gat act agg ggc aaa cga gac aga gaa aag gac tca      1656
161 Glu Arg Arg Glu Asp Thr Arg Gly Lys Arg Asp Arg Glu Lys Asp Ser
162 415      420      425      430
164 aga gaa gaa cga gaa tat gaa cag gat cag agc tct tct aga gac cac      1704
165 Arg Glu Glu Arg Glu Tyr Glu Gln Asp Gln Ser Ser Ser Arg Asp His
166      435      440      445
168 aga gat gac aga gaa cct cga gat ggt cgg gat cgg aga gat gcc aga      1752
169 Arg Asp Asp Arg Glu Pro Arg Asp Gly Arg Asp Arg Arg Asp Ala Arg
170      450      455      460
172 gat act agg gac cga agg gaa cta aga gac tcc aga gac atg cgg gac      1800
173 Asp Thr Arg Asp Arg Arg Glu Leu Arg Asp Ser Arg Asp Met Arg Asp
174      465      470      475
176 tca agg gag atg aga gat tat agc aga gat acc aaa gag agc cgt gat      1848
177 Ser Arg Glu Met Arg Asp Tyr Ser Arg Asp Thr Lys Glu Ser Arg Asp
178      480      485      490
180 ccc aga gat tct cgg tcc act cgt gat gcc cat gac tac agg gac cgt      1896
181 Pro Arg Asp Ser Arg Ser Thr Arg Asp Ala His Asp Tyr Arg Asp Arg
182 495      500      505      510
184 gaa ggt cga gat act cat cga aag gag gat aca tat cca gaa gaa tcc      1944
185 Glu Gly Arg Asp Thr His Arg Lys Glu Asp Thr Tyr Pro Glu Glu Ser
186      515      520      525
188 cgg agt tat ggc cga aac cat ttg aga gaa gaa agt tct cgt acg gaa      1992
189 Arg Ser Tyr Gly Arg Asn His Leu Arg Glu Glu Ser Ser Arg Thr Glu
190      530      535      540
192 ata agg aat gag tcc aga aat gag tct cga agt gaa att aga aat gac      2040
193 Ile Arg Asn Glu Ser Arg Asn Glu Ser Arg Ser Glu Ile Arg Asn Asp
194      545      550      555
196 cga atg ggc cga agt agg ggg agg gtt cct gag tta cct gaa aag gga      2088
197 Arg Met Gly Arg Ser Arg Gly Arg Val Pro Glu Leu Pro Glu Lys Gly

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201	Ser Arg Gly Ser Arg Gly Ser Gln Ile Asp Ser His Ser Ser Asn Ser			
202	575 580 585 590			
204	aac tat cat gac agc tgg gaa act cga agt agc tat cct gaa aga gat	2184		
205	Asn Tyr His Asp Ser Trp Glu Thr Arg Ser Ser Tyr Pro Glu Arg Asp			
206	595 600 605			
208	aga tat cct gaa aga gac aac aga gat caa gca agg gat tct tcc ttt	2232		
209	Arg Tyr Pro Glu Arg Asp Asn Arg Asp Gln Ala Arg Asp Ser Ser Phe			
210	610 615 620			
212	gag aga aga cat gga gag cga gac cgt cgt gac aac aga gag aga gat	2280		
213	Glu Arg Arg His Gly Glu Arg Asp Arg Arg Asp Asn Arg Glu Arg Asp			
214	625 630 635			
216	caa aga cca agc tca cca att cga cat cag gga agg aat gac gag ctt	2328		
217	Gln Arg Pro Ser Ser Pro Ile Arg His Gln Gly Arg Asn Asp Glu Leu			
218	640 645 650			
220	gag cgt gat gaa aga aga gag gaa cga aga gta gac aga gtg gat gat	2376		
221	Glu Arg Asp Glu Arg Arg Glu Glu Arg Arg Val Asp Arg Val Asp Asp			
222	655 660 665 670			
224	agg aga gat gaa agg gct aga gag aga gat cgg gaa cga gaa cga gac	2424		
225	Arg Arg Asp Glu Arg Ala Arg Glu Arg Asp Arg Glu Arg Glu Arg Asp			
226	675 680 685			
228	agg gag cgg gag aga gag agg gaa cgt gaa cgg gat cgg gaa aga gaa	2472		
229	Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Glu			
230	690 695 700			
232	aaa gag aga gaa cta gaa aga gag cgt gct agg gaa cgg gag aga gaa	2520		
233	Lys Glu Arg Glu Leu Glu Arg Glu Arg Ala Arg Glu Arg Glu Arg Glu			
234	705 710 715			
236	aga gaa aaa gag aga gat cgt gaa agg gat aga gac cga gac cac gat	2568		
237	Arg Glu Lys Glu Arg Asp Arg Glu Arg Asp Arg Asp Arg Asp His Asp			
238	720 725 730			
240	cga gag cgg gaa aga gag agg gaa cga gac agg gaa aaa gaa cgg gaa	2616		
241	Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Lys Glu Arg Glu			
242	735 740 745 750			
244	cga gaa aga gaa gag aga gag agg gag aga gag cga gaa cgg gag aga	2664		
245	Arg Glu Arg Glu Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg			
246	755 760 765			
248	gag cga gag cga gaa cgg gaa cga gaa aga gcg aga gaa agg gat aaa	2712		
249	Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Ala Arg Glu Arg Asp Lys			
250	770 775 780			
252	gaa cga gaa cgc caa agg gat tgg gaa gac aaa gac aaa gga cga gat	2760		
253	Glu Arg Glu Arg Gln Arg Asp Trp Glu Asp Lys Asp Lys Gly Arg Asp			
254	785 790 795			
256	gac cgc aga gaa aag cga gaa gag atc cga gaa gat agg aat cca aga	2808		
257	Asp Arg Arg Glu Lys Arg Glu Glu Ile Arg Glu Asp Arg Asn Pro Arg			
258	800 805 810			
260	gat gga cat gat gaa aga aaa tca aag aag cgc tat aga aat gaa ggg	2856		
261	Asp Gly His Asp Glu Arg Lys Ser Lys Lys Arg Tyr Arg Asn Glu Gly			
262	815 820 825 830			

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264 agt ccc agc cct aga cag tcc ccg aag cgc cgg cgt gaa cat tct ccg      2904
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266           835           840           845
268 gac agt gat gcc tac aac agt gga gat gat aaa aat gaa aaa cac aga      2952
269 Asp Ser Asp Ala Tyr Asn Ser Gly Asp Asp Lys Asn Glu Lys His Arg
270           850           855           860
272 ctc ttg agc caa gtt gta cga cct caa gaa tct cgt tct ctt agt ccc      3000
273 Leu Leu Ser Gln Val Val Arg Pro Gln Glu Ser Arg Ser Leu Ser Pro
274           865           870           875
276 tcg cac ctc aca gaa gac aga cag ggt aga tgg aaa gag gag gat cgt      3048
277 Ser His Leu Thr Glu Asp Arg Gln Gly Arg Trp Lys Glu Glu Asp Arg
278           880           885           890
280 aaa cca gaa agg aaa gag agt tca agg cgc tac gaa gaa cag gaa ctc      3096
281 Lys Pro Glu Arg Lys Glu Ser Ser Arg Arg Tyr Glu Glu Gln Glu Leu
282 895           900           905           910
284 aag gag aaa gtt tct tct gta gat aaa cag aga gaa cag aca gaa atc      3144
285 Lys Glu Lys Val Ser Ser Val Asp Lys Gln Arg Glu Gln Thr Glu Ile
286           915           920           925
288 ctg gaa agc tca aga atg cgt gca cag gac att ata gga cac cac cag      3192
289 Leu Glu Ser Ser Arg Met Arg Ala Gln Asp Ile Ile Gly His His Gln
290           930           935           940
292 tct gaa gat cga gag aca tct gat cga gct cat gat gaa aac aag aag      3240
293 Ser Glu Asp Arg Glu Thr Ser Asp Arg Ala His Asp Glu Asn Lys Lys
294           945           950           955
296 aaa gca aaa att caa aag aaa cca att aag aaa aag aaa gag gat gat      3288
297 Lys Ala Lys Ile Gln Lys Lys Pro Ile Lys Lys Lys Lys Glu Asp Asp
298           960           965           970
300 gtt gga ata gag agg ggt aac ata gag aca aca tct gaa gat ggt caa      3336
301 Val Gly Ile Glu Arg Gly Asn Ile Glu Thr Thr Ser Glu Asp Gly Gln
302 975           980           985           990
304 gta ttt tca cca aaa aaa gga cag aaa aag aaa agc att gaa aaa aaa      3384
305 Val Phe Ser Pro Lys Lys Gly Gln Lys Lys Lys Ser Ile Glu Lys Lys
306           995           1000           1005
308 cgt aaa aaa tcc aaa ggt gat tct gat att tct gat gaa gaa gca      3429
309 Arg Lys Lys Ser Lys Gly Asp Ser Asp Ile Ser Asp Glu Glu Ala
310           1010           1015           1020
312 gcc cag caa agt aag aag aaa aga ggc cca cgg act ccc cct ata      3474
313 Ala Gln Gln Ser Lys Lys Lys Arg Gly Pro Arg Thr Pro Pro Ile
314           1025           1030           1035
316 aca act aaa gag gaa ttg gtt gaa atg tgc aat ggt aag aat ggt      3519
317 Thr Thr Lys Glu Glu Leu Val Glu Met Cys Asn Gly Lys Asn Gly
318           1040           1045           1050
320 att cta gag gac tcc cag aaa aaa gaa gat aca gca ttc agt gac      3564
321 Ile Leu Glu Asp Ser Gln Lys Lys Glu Asp Thr Ala Phe Ser Asp
322           1055           1060           1065
324 tgg tct gat gag gat gtc cct gac cgt aca gag gtg aca gaa gca      3609
325 Trp Ser Asp Glu Asp Val Pro Asp Arg Thr Glu Val Thr Glu Ala
326           1070           1075           1080
328 gag cat act gcc acc gcc acg act cct ggt agt acc cct tct cct      3654

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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